

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/553,661

CRF Edit Date: 11/1/05
Edited by: M

— Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

— Corrected the SEQ ID NO. Sequence numbers edited were:

— Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

— Deleted invalid beginning/end-of-file text ; page numbers

— Inserted mandatory headings/numeric identifiers, specifically:

— Moved responses to same line as heading/numeric identifier, specifically:

— Other:



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,661

DATE: 11/01/2005

TIME: 11:57:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11012005\J553661.raw

3 <110> APPLICANT: Genesis Group Inc., Kenneth Kao, Catherine Popadiuk
 5 <120> TITLE OF INVENTION: Pygopus in Diagnosis and Treatment of Cancer
 7 <130> FILE REFERENCE: 50680-4
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/553,661
 C--> 9 <141> CURRENT FILING DATE: 2005-10-17
 9 <150> PRIOR APPLICATION NUMBER: US 60/463 309
 10 <151> PRIOR FILING DATE: 2003-04-17
 12 <150> PRIOR APPLICATION NUMBER: US 60/496 012
 13 <151> PRIOR FILING DATE: 2003-08-19
 15 <160> NUMBER OF SEQ ID NOS: 28
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3190
 21 <212> TYPE: DNA
 22 <213> ORGANISM: homosapiens
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: hPygo-2
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (173)..(1393)
 31 <400> SEQUENCE: 1
 32 gtctggagag agcgcgcagt ttgcgcggcg gctcggcgct tccctgtcggt cgcactttgt 60
 34 ggttgctgca gctcgggggc ctgggctgcc cctgacacccc cttctggcg atggtgca 120
 36 ccaagggcgc ctccatcccc cgccgctgcc gctaaccgg gtcccccact cc atg gcc 178
 37 Met Ala
 38 1
 40 gcc tcg gcg ccc cca ccg gac aag ctg gag gga ggt ggc ggc ccc 226
 41 Ala Ser Ala Pro Pro Pro Pro Asp Lys Leu Glu Gly Gly Gly Pro
 42 5 10 15
 44 gca ccg ccc cct gcg ccc agc acc ggg agg aag cag ggc aag gcc 274
 45 Ala Pro Pro Pro Ala Pro Pro Ser Thr Gly Arg Lys Gln Gly Lys Ala
 46 20 25 30
 48 ggt ctg caa atg aag agt cca gaa aag aag cga agg aag tca aat act 322
 49 Gly Leu Gln Met Lys Ser Pro Glu Lys Lys Arg Arg Lys Ser Asn Thr
 50 35 40 45 50
 52 cag ggc cct gca tac tca cat ctg acg gag ttt gca cca ccc cca act 370
 53 Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro Pro Thr
 54 55 60 65
 57 ccc atg gtg gat cac ctg gtt gca tcc aac cct ttt gaa gat gac ttc 418
 58 Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp Asp Phe
 59 70 75 80
 61 gga gcc ccc aaa gtg ggg gtt gca gcc cct cca ttc ctt ggc agt cct 466
 62 Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly Ser Pro

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63	85	90	95	
65	gtg ccc ttc gga ggc ttc cgt gtg cag ggg ggc atg gcg ggc cag gta			514
66	Val Pro Phe Gly Gly Phe Arg Val Gln Gly Gly Met Ala Gly Gln Val			
67	100	105	110	
69	ccc cca ggc tac agc act gga ggt gga ggg ggc ccc cag cca ctc cgt			562
70	Pro Pro Gly Tyr Ser Thr Gly Gly Gly Pro Gln Pro Leu Arg			
71	115	120	125	130
73	cga cag cca ccc ccc ttc cct ccc aat cct atg ggc cct gct ttc aac			610
74	Arg Gln Pro Pro Phe Pro Pro Asn Pro Met Gly Pro Ala Phe Asn			
75	135	140	145	
77	atg ccc ccc cag ggt cct ggc tac cca ccc cca ggc aac atg aac ttt			658
78	Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly Asn Met Asn Phe			
79	150	155	160	
81	ccc agc caa ccc ttc aac cag cct ctg ggt caa aac ttt agt cct ccc			706
82	Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn Phe Ser Pro Pro			
83	165	170	175	
85	agt ggg cag atg atg ccg ggc cca gtg ggg gga ttt ggt ccc atg atc			754
86	Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe Gly Pro Met Ile			
87	180	185	190	
89	tca ccc acc atg gga cag cct ccc aga gca gag ctg ggc cca cct tct			802
90	Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu Leu Gly Pro Pro Ser			
91	195	200	205	210
93	ctg tcc caa cga ttt gct cag cca ggg gct cct ttt ggc cct tct cct			850
94	Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe Gly Pro Ser Pro			
95	215	220	225	
97	ctc cag aga cct ggt cag ggg ctc ccc agc ctg ccg cct aac aca agt			898
98	Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro Pro Asn Thr Ser			
99	230	235	240	
101	ccc ttt cct ggt ccg gac cct ggc ttt cct ggc cct ggt ggt gag gat			946
102	Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly Pro Gly Glu Asp			
103	245	250	255	
105	ggg ggg aag ccc ttg aat cca cct gct tct act gct ttt ccc cag gag			994
106	Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr Ala Phe Pro Gln Glu			
107	260	265	270	
109	ccc cac tca ggc tcc ccg gct gct gtt aat ggg aac cag ccc agt			1042
110	Pro His Ser Gly Ser Pro Ala Ala Ala Val Asn Gly Asn Gln Pro Ser			
111	275	280	285	290
114	ttc ccc ccg aac agc agt ggg cgg ggt ggg ggc act cca gat gcc aac			1090
115	Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Thr Pro Asp Ala Asn			
116	295	300	305	
118	agc ttg gca ccc cct ggc aag gca ggt ggg ggc tcc ggg ccc cag cct			1138
119	Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Ser Gly Pro Gln Pro			
120	310	315	320	
122	ccc cca ggc ttg gtg tac cca tgt ggt gcc tgt cgg agt gag gtg aac			1186
123	Pro Pro Gly Leu Val Tyr Pro Cys Gly Ala Cys Arg Ser Glu Val Asn			
124	325	330	335	
126	gat gac cag gat gcc att ctg tgt gag gcc tcc tgc cag aaa tgg ttc			1234
127	Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys Trp Phe			
128	340	345	350	

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Input Set : A:\PTO.AMC.txt
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130 cac cgt gag tgc aca ggc atg act gag agc gcc tat ggg ctg ctg acc	1282
131 His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu Leu Thr	
132 355 360 365 370	
134 act gaa gct tct gcc gtc tgg gcc tgc gat ctc tgc ctc aag acc aag	1330
135 Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys Thr Lys	
136 375 380 385	
138 gag atc cag tct gtc tac atc cgt gag ggc atg ggg cag ctg gtg gct	1378
139 Glu Ile Gln Ser Val Tyr Ile Arg Glu Gly Met Gly Gln Leu Val Ala	
140 390 395 400	
142 gct aac gat ggg tga cgctggtaa gtggccagg gaagtgcaca tgtctctccc	1433
143 Ala Asn Asp Gly	
144 405	
146 tgctttcca gggtgatttt ttgtatgttt ggcttgggt cttgtttcc actggcttc	1493
147 catccccatg gggcagaaac agtggctcct gggagcagaa aaggaattga ggtggcagg	1553
148 cagaagagcc tggattgctc actgtttgg gaaacttaca tggatgtttt tacagagatc	1613
149 caggaaacca aagccctgtt gggcagagcc attttgtggc tatttctgga gcccaggag	1673
150 tggatgttca agagaaaagg ggctggagaa agatccggag ggcagggtt ttcctctgc	1733
151 tggatgttca acctgtgcct aacaccccta ctgaacccca cagctccagc	1793
152 cttatgtttt ggagtcaagt gttaaagggtt tctggccaga ggaattgggg tcttgcata	1853
153 cctgcaatag ccctttatg ggctctggaa gacagctta gggataaat gggattttc	1913
154 cccttttct acccactcct ttgcttcctc caagacttac ccaactcctt cccctcaga	1973
155 gaaccaaata gcctgaggaa gcaggagat tcctggttat ggcagtttct tggatgtt	2033
156 ggccttcaag acatggatgtt agagatgtt tcaggacgta tcttcttcat accaaagtca	2093
157 ctggatgtt ctcagctct ctcgtgttt tctcttcatg accatattt tgccaaaaat	2153
158 tggatgtt tatctgacag accagaatat ttgaagtttggctgtcctt aaagtctgg	2213
159 ctggatgtt acccttcctcc cccagccat ctgtgcaca ttatactccg tggatgtt	2273
160 aactttcgcc gcccattttt ccctgccttc ctggcttcatg tgaaggaaag cttgaaaagg	2333
161 cgcagagccc tataccat ttcctccatg ataaaaggat ccaagtggagg ccctgtcaca	2393
162 gcctgtgggt agggatgcg gcgggatcctt cattgccatg gtactcaaag gttagaagagc	2453
163 ctggatgtt ttgcttctt ttgttattttt ttcataatcctt cttggccctg gtgattaatt	2513
164 agcaattctc attcctctca gccaaaggcc tgcactggc tttatgttgc tttttttttt	2573
165 tttaagcac tgcctgtccag agatgggcctt ggggctgtat gaggaccta tgcgtgtcg	2633
166 ttctcccttt ctgttcatgc acacattcctt ccatgggtt gggaggccat gcatgggtt	2693
167 tggccctcg agaagtttgg agtccccccat ctcaagatac agtggcaag acctatgtgt	2753
168 cccctacccc cacttctctc agttcctggc atgaggagag aagaccctgc tctggtgag	2813
169 ctgacaacct ttgaggctgg gaggagaga gcctctggc atcgatccca gtgtccctca	2873
170 cactaaaacg gcgttagatgg caacccccc cccccacccc gctgtcaac tcttgtt	2933
171 gttgttctgt ttggccattt tatctgttgc tggatgttgc ttgttccctt ctgtccgca	2993
172 tttgtaaaaa ttggccctgg gggatgttt ttgttggatc tgctccctt cgctctctca	3053
173 ctccactact tttgtacaa agtgtatggca gaatgcgggtt gtggatgggg tctttgtac	3113
174 tggatgtt ataaaatgtt tttttttttt caaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa	3173
175 aaaaaaaaaaaa aaaaaaaaaaaa	3190
178 <210> SEQ ID NO: 2	
179 <211> LENGTH: 406	
180 <212> TYPE: PRT	
181 <213> ORGANISM: homosapiens	
183 <220> FEATURE:	
184 <223> OTHER INFORMATION: hPygo-2	
186 <400> SEQUENCE: 2	

RAW SEQUENCE LISTING
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188 Met Ala Ala Ser Ala Pro Pro Pro Asp Lys Leu Glu Gly Gly Gly
189 1 5 10 15
191 Gly Pro Ala Pro Pro Pro Ala Pro Pro Ser Thr Gly Arg Lys Gln Gly
192 20 25 30
194 Lys Ala Gly Leu Gln Met Lys Ser Pro Glu Lys Lys Arg Arg Lys Ser
195 35 40 45
197 Asn Thr Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro
198 50 55 60
200 Pro Thr Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp
201 65 70 75 80
203 Asp Phe Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly
204 85 90 95
206 Ser Pro Val Pro Phe Gly Gly Phe Arg Val Gln Gly Gly Met Ala Gly
207 100 105 110
209 Gln Val Pro Pro Gly Tyr Ser Thr Gly Gly Gly Gly Pro Gln Pro
210 115 120 125
212 Leu Arg Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro Met Gly Pro Ala
213 130 135 140
215 Phe Asn Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly Asn Met
216 145 150 155 160
218 Asn Phe Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn Phe Ser
219 165 170 175
221 Pro Pro Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe Gly Pro
222 180 185 190
224 Met Ile Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu Leu Gly Pro
225 195 200 205
228 Pro Ser Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe Gly Pro
229 210 215 220
231 Ser Pro Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro Pro Asn
232 225 230 235 240
234 Thr Ser Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly Pro Gly Gly
235 245 250 255
237 Glu Asp Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr Ala Phe Pro
238 260 265 270
240 Gln Glu Pro His Ser Gly Ser Pro Ala Ala Ala Val Asn Gly Asn Gln
241 275 280 285
243 Pro Ser Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Thr Pro Asp
244 290 295 300
246 Ala Asn Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Ser Gly Pro
247 305 310 315 320
249 Gln Pro Pro Pro Gly Leu Val Tyr Pro Cys Gly Ala Cys Arg Ser Glu
250 325 330 335
252 Val Asn Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys
253 340 345 350
255 Trp Phe His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu
256 355 360 365
258 Leu Thr Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys
259 370 375 380
261 Thr Lys Glu Ile Gln Ser Val Tyr Ile Arg Glu Gly Met Gly Gln Leu

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Input Set : A:\PTO.AMC.txt
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262	385	390	395	400
264	Val Ala Ala Asn Asp Gly			
265		405		
268	<210> SEQ ID NO: 3			
269	<211> LENGTH: 1260			
270	<212> TYPE: DNA			
271	<213> ORGANISM: homosapiens			
273	<220> FEATURE:			
274	<221> NAME/KEY: CDS			
275	<222> LOCATION: (1)..(1260)			
277	<220> FEATURE:			
278	<223> OTHER INFORMATION: hPygo-1			
280	<400> SEQUENCE: 3			
281	atg ccc gcc gag aac tct cca gct ccc gct tac aaa gtt tcc tcg cat			48
282	Met Pro Ala Glu Asn Ser Pro Ala Pro Ala Tyr Lys Val Ser Ser His			
283	1 5 10 15			
285	ggt ggt gat agt gga ctg gat ggg tta gga gga cca ggt gta caa cta			96
286	Gly Gly Asp Ser Gly Leu Asp Gly Leu Gly Gly Pro Gly Val Gln Leu			
287	20 25 30			
289	gga agc cca gat aag aaa aag cgc aag gca aat aca cag gga cct tct			144
290	Gly Ser Pro Asp Lys Lys Arg Lys Ala Asn Thr Gln Gly Pro Ser			
291	35 40 45			
293	tcc cct cca ttg tct gag tat gct cca cca ccg aat cca aac tct gac			192
294	Phe Pro Pro Leu Ser Glu Tyr Ala Pro Pro Asn Pro Asn Ser Asp			
295	50 55 60			
297	cat cta gtg gct gct aat cca ttt gat gac aac tat aat act att tcc			240
298	His Leu Val Ala Ala Asn Pro Phe Asp Asp Asn Tyr Asn Thr Ile Ser			
299	65 70 75 80			
301	tat aaa cca cta cct tcg tca aat cca tat ctt ggc cct ggt tat cct			288
302	Tyr Lys Pro Leu Pro Ser Ser Asn Pro Tyr Leu Gly Pro Gly Tyr Pro			
303	85 90 95			
305	ggc ttt gga ggc tat agt aca ttc aga atg cca cct cac gtt ccc cca			336
306	Gly Phe Gly Gly Tyr Ser Thr Phe Arg Met Pro Pro His Val Pro Pro			
307	100 105 110			
309	aga atg tct tcc cca tac tgt ggt cct tac tca ctc agg aac cag cca			384
310	Arg Met Ser Ser Pro Tyr Cys Gly Pro Tyr Ser Leu Arg Asn Gln Pro			
311	115 120 125			
313	cac cca ttt cct cag aat cct ctg ggc atg ggt ttt aat cga cct cat			432
314	His Pro Phe Pro Gln Asn Pro Leu Gly Met Gly Phe Asn Arg Pro His			
315	130 135 140			
317	gct ttt aac ttt ggg cca cat gat aat tca agt ttc ggt aat cca tct			480
318	Ala Phe Asn Phe Gly Pro His Asp Asn Ser Ser Phe Gly Asn Pro Ser			
319	145 150 155 160			
321	tat aat aat gca cta agt cag aat gtc aac atg cct aat caa cat ttt			528
322	Tyr Asn Asn Ala Leu Ser Gln Asn Val Asn Met Pro Asn Gln His Phe			
323	165 170 175			
325	aga caa aat cct gct gaa aat ttc agt caa att cct cca cag aat gct			576
326	Arg Gln Asn Pro Ala Glu Asn Phe Ser Gln Ile Pro Pro Gln Asn Ala			
327	180 185 190			

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28

VERIFICATION SUMMARY
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date